



IFWO

**RAW SEQUENCE LISTING**

DATE: 09/17/2004

PATENT APPLICATION: US/10/788,992

TIME: 08:55:02

Input Set : N:\Crf3\RULE60\10788992.raw.txt  
 Output Set: N:\CRF4\09172004\J788992.raw

**SEQUENCE LISTING**

- 3 (1) GENERAL INFORMATION:
  - 5 (i) APPLICANT: Gilula, Norton B  
Cravatt, Benjamin F  
Lerner, Richard A
  - 9 (ii) TITLE OF INVENTION: FATTY-ACID AMIDE HYDROLASE
  - 11 (iii) NUMBER OF SEQUENCES: 54
  - 13 (iv) CORRESPONDENCE ADDRESS:
    - 14 (A) ADDRESSEE: The Scripps Research Institute
    - 15 (B) STREET: 10550 North Torrey Pines Road
    - 16 (C) CITY: La Jolla
    - 17 (D) STATE: California
    - 18 (E) COUNTRY: US
    - 19 (F) ZIP: 92037
  - 21 (v) COMPUTER READABLE FORM:
    - 22 (A) MEDIUM TYPE: Floppy disk
    - 23 (B) COMPUTER: IBM PC compatible
    - 24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - 25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
  - 27 (vi) CURRENT APPLICATION DATA:
    - 28 (A) APPLICATION NUMBER: US/10/788,992
    - 29 (B) FILING DATE: 26-Feb-2004
    - 30 (C) CLASSIFICATION: 435
  - 32 (vii) PRIOR APPLICATION DATA:
    - 33 (A) APPLICATION NUMBER: US/08/743,168
    - 34 (B) FILING DATE: 01-May-1998
    - 35 (A) APPLICATION NUMBER: US 08/489,535
    - 36 (B) FILING DATE: 12-JUN-1995
  - 38 (viii) ATTORNEY/AGENT INFORMATION:
    - 39 (A) NAME: Fitting, Thomas
    - 40 (B) REGISTRATION NUMBER: 34,163
    - 41 (C) REFERENCE/DOCKET NUMBER: TSRI 485.2
  - 43 (ix) TELECOMMUNICATION INFORMATION:
    - 44 (A) TELEPHONE: (619) 784-2937
    - 45 (B) TELEFAX: (619) 784-9399
  - 48 (2) INFORMATION FOR SEQ ID NO: 1:
    - 50 (i) SEQUENCE CHARACTERISTICS:
      - 51 (A) LENGTH: 783 base pairs
      - 52 (B) TYPE: nucleic acid
      - 53 (C) STRANDEDNESS: double
      - 54 (D) TOPOLOGY: linear
    - 56 (ii) MOLECULE TYPE: cDNA
    - 58 (iii) HYPOTHETICAL: NO

**ENTERED**

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/788,992

DATE: 09/17/2004

TIME: 08:55:02

Input Set : N:\Crf3\RULE60\10788992.raw.txt  
 Output Set: N:\CRF4\09172004\J788992.raw

60       (iv) ANTI-SENSE: NO  
 63       (ix) FEATURE:  
 64           (A) NAME/KEY: CDS  
 65           (B) LOCATION: 1..783  
 68       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 70 AGC CCA GGA GGT TCC TCA GGG GGT GAG GGG GCT CTC ATT GGA TCT GGA           48  
 71 Ser Pro Gly Gly Ser Ser Gly Gly Glu Ala Leu Ile Gly Ser Gly  
 72     1               5               10               15  
 74 GGT TCC CCT CTG GGT TTA GGC ACT GAC ATT GGC GGC AGC ATC CGG TTC           96  
 75 Gly Ser Pro Leu Gly Leu Gly Thr Asp Ile Gly Gly Ser Ile Arg Phe  
 76     20               25               30  
 78 CCT TCT GCC TTC TGC GGC ATC TGT GGC CTC AAG CCT ACT GGC AAC CGC           144  
 79 Pro Ser Ala Phe Cys Gly Ile Cys Gly Leu Lys Pro Thr Gly Asn Arg  
 80     35               40               45  
 82 CTC AGC AAG AGT GGC CTG AAG GGC TGT GTC TAT GGA CAG ACG GCA GTG           192  
 83 Leu Ser Lys Ser Gly Leu Lys Gly Cys Val Tyr Gly Gln Thr Ala Val  
 84     50               55               60  
 86 CAG CTT TCT CTT GGC CCC ATG GCC CGG GAT GTG GAG AGC CTG GCG CTA           240  
 87 Gln Leu Ser Leu Gly Pro Met Ala Arg Asp Val Glu Ser Leu Ala Leu  
 88     65               70               75               80  
 90 TGC CTG AAA GCT CTA CTG TGT GAG CAC TTG TTC ACC TTG GAC CCT ACC           288  
 91 Cys Leu Lys Ala Leu Leu Cys Glu His Leu Phe Thr Leu Asp Pro Thr  
 92     85               90               95  
 94 GTG CCT CCC TTT CCC TTC AGA GAG GAG GTC TAT AGA AGT TCT AGA CCC           336  
 95 Val Pro Pro Phe Pro Arg Glu Glu Val Tyr Arg Ser Ser Arg Pro  
 96     100              105              110  
 98 CTG CGT GTG GGG TAC TAT GAG ACT GAC AAC TAT ACC ATG CCC AGC CCA           384  
 99 Leu Arg Val Gly Tyr Tyr Glu Thr Asp Asn Tyr Thr Met Pro Ser Pro  
 100     115              120              125  
 102 GCT ATG AGG AGG GCT CTG ATA GAG ACC AAG CAG AGA CTT GAG GCT GCT           432  
 103 Ala Met Arg Arg Ala Leu Ile Glu Thr Lys Gln Arg Leu Glu Ala Ala  
 104     130              135              140  
 106 GGC CAC ACG CTG ATT CCC TTC TTA CCC AAC AAC ATA CCC TAC GCC CTG           480  
 107 Gly His Thr Leu Ile Pro Phe Leu Pro Asn Asn Ile Pro Tyr Ala Leu  
 108     145              150              155              160  
 110 GAG GTC CTG TCT GCG GGC GGC CTG TTC AGT GAC GGT GGC CGC AGT TTT           528  
 111 Glu Val Leu Ser Ala Gly Gly Leu Phe Ser Asp Gly Gly Arg Ser Phe  
 112     165              170              175  
 114 CTC CAA AAC TTC AAA GGT GAC TTT GTG GAT CCC TGC TTG GGA GAC CTG           576  
 115 Leu Gln Asn Phe Lys Gly Asp Phe Val Asp Pro Cys Leu Gly Asp Leu  
 116     180              185              190  
 118 ATC TTA ATT CTG AGG CTG CCC AGC TGG TTT AAA AGA CTG CTG AGC CTC           624  
 119 Ile Leu Ile Leu Arg Leu Pro Ser Trp Phe Lys Arg Leu Leu Ser Leu  
 120     195              200              205  
 122 CTG CTG AAG CCT CTG TTT CCT CGG CTG GCA GCC TTT CTC AAC AGT ATG           672  
 123 Leu Leu Lys Pro Leu Phe Pro Arg Leu Ala Ala Phe Leu Asn Ser Met  
 124     210              215              220  
 126 CGT CCT CGG TCA GCT GAA AAG CTG TGG AAA CTG CAG CAT GAG ATT GAG           720  
 127 Arg Pro Arg Ser Ala Glu Lys Leu Trp Lys Leu Gln His Glu Ile Glu

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/788,992

DATE: 09/17/2004

TIME: 08:55:02

Input Set : N:\Crf3\RULE60\10788992.raw.txt  
 Output Set: N:\CRF4\09172004\J788992.raw

128	225	230	235	240	
130	ATG TAT CGC CAG TCT GTG ATT GCC CAG TGG AAA GCG ATG AAC TTG GAT				768
131	Met Tyr Arg Gln Ser Val Ile Ala Gln Trp Lys Ala Met Asn Leu Asp				
132	245	250	255		
134	GTG CTG CTG ACC TAA				783
135	Val Leu Leu Thr				
136	260				
139	(2) INFORMATION FOR SEQ ID NO: 2:				
141	(i) SEQUENCE CHARACTERISTICS:				
142	(A) LENGTH: 260 amino acids				
143	(B) TYPE: amino acid				
144	(D) TOPOLOGY: linear				
146	(ii) MOLECULE TYPE: protein				
148	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:				
150	Ser Pro Gly Gly Ser Ser Gly Gly Glu Gly Ala Leu Ile Gly Ser Gly				
151	1	5	10	15	
153	Gly Ser Pro Leu Gly Leu Gly Thr Asp Ile Gly Gly Ser Ile Arg Phe				
154	20	25	30		
156	Pro Ser Ala Phe Cys Gly Ile Cys Gly Leu Lys Pro Thr Gly Asn Arg				
157	35	40	45		
159	Leu Ser Lys Ser Gly Leu Lys Gly Cys Val Tyr Gly Gln Thr Ala Val				
160	50	55	60		
162	Gln Leu Ser Leu Gly Pro Met Ala Arg Asp Val Glu Ser Leu Ala Leu				
163	65	70	75	80	
165	Cys Leu Lys Ala Leu Leu Cys Glu His Leu Phe Thr Leu Asp Pro Thr				
166	85	90	95		
168	Val Pro Pro Phe Pro Phe Arg Glu Glu Val Tyr Arg Ser Ser Arg Pro				
169	100	105	110		
171	Leu Arg Val Gly Tyr Tyr Glu Thr Asp Asn Tyr Thr Met Pro Ser Pro				
172	115	120	125		
174	Ala Met Arg Arg Ala Leu Ile Glu Thr Lys Gln Arg Leu Glu Ala Ala				
175	130	135	140		
177	Gly His Thr Leu Ile Pro Phe Leu Pro Asn Asn Ile Pro Tyr Ala Leu				
178	145	150	155	160	
180	Glu Val Leu Ser Ala Gly Gly Leu Phe Ser Asp Gly Gly Arg Ser Phe				
181	165	170	175		
183	Leu Gln Asn Phe Lys Gly Asp Phe Val Asp Pro Cys Leu Gly Asp Leu				
184	180	185	190		
186	Ile Leu Ile Leu Arg Leu Pro Ser Trp Phe Lys Arg Leu Leu Ser Leu				
187	195	200	205		
189	Leu Leu Lys Pro Leu Phe Pro Arg Leu Ala Ala Phe Leu Asn Ser Met				
190	210	215	220		
192	Arg Pro Arg Ser Ala Glu Lys Leu Trp Lys Leu Gln His Glu Ile Glu				
193	225	230	235	240	
195	Met Tyr Arg Gln Ser Val Ile Ala Gln Trp Lys Ala Met Asn Leu Asp				
196	245	250	255		
198	Val Leu Leu Thr				
199	260				
202	(2) INFORMATION FOR SEQ ID NO: 3:				

**RAW SEQUENCE LISTING**

PATENT APPLICATION: US/10/788,992

DATE: 09/17/2004

TIME: 08:55:02

Input Set : N:\CrF3\RULE60\10788992.raw.txt  
Output Set: N:\CRF4\09172004\J788992.raw

204 (i) SEQUENCE CHARACTERISTICS:  
205 (A) LENGTH: 22 base pairs  
206 (B) TYPE: nucleic acid  
207 (C) STRANDEDNESS: single  
208 (D) TOPOLOGY: linear  
210 (ii) MOLECULE TYPE: cDNA  
212 (iii) HYPOTHETICAL: NO  
214 (iv) ANTI-SENSE: NO  
218 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

22

222 (2) INFORMATION FOR SEQ ID NO: 4:  
223 (i) SEQUENCE CHARACTERISTICS:  
224 (A) LENGTH: 5 amino acids  
225 (B) TYPE: amino acid  
226 (C) TOPOLOGY: linear  
227 (ii) MOLECULE TYPE: peptide  
228 (v) FRAGMENT TYPE: internal  
229 (xi) SEQUENCE DESCRIPTION: SEQ

237 Gly Gly Glu Gly Ala  
238 1 5

240 (2) INFORMATION FOR SEQ ID NO: 5:  
242 (i) SEQUENCE CHARACTERISTICS:  
243 (A) LENGTH: 31 amino acids  
244 (B) TYPE: amino acid  
245 (D) TOPOLOGY: linear  
247 (ii) MOLECULE TYPE: peptide  
249 (v) FRAGMENT TYPE: internal  
252 (vi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

253 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
 255 Gly Gly Ser Ser Gly Gly Glu Gly Ala Leu Ile Gly Ser Gly Gly Ser  
 256 1 5 10 15  
 258 Pro Leu Gly Leu Gly Thr Asp Ile Gly Gly Ser Ile Arg Phe Pro  
 259 20 25 30

261 (2) INFORMATION FOR SEQ ID NO: 6:

263 (i) SEQUENCE CHARACTERISTICS:  
264 (A) LENGTH: 15 amino acids  
265 (B) TYPE: amino acid  
266 (D) TOPOLOGY: linear  
268 (ii) MOLECULE TYPE: peptide  
270 (v) FRAGMENT TYPE: internal

274 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

276 Ser Pro Gly Gly Ser Ser Gly Gly Glu Gly Ala Leu Ile Gly Ser  
277 1 5 10 15  
278 (a) INFORMATION FOR SEQ ID NO: 3.

279 (2) INFORMATION FOR SEQ ID NO: 7:  
280 (A) MDA

281 (i) SEQUENCE CHARACTERISTICS:  
282 (A) LENGTH: 15 amino acids  
283 (B) TYPE: amino acid  
284 (D) TOPOLOGY: linear  
285 (ii) MOLECULE TYPE: peptide  
286 (v) FRAGMENT TYPE: intact

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/788,992

DATE: 09/17/2004

TIME: 08:55:02

Input Set : N:\Crf3\RULE60\10788992.raw.txt  
Output Set: N:\CRF4\09172004\J788992.raw

292 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
294 Ala Leu Ile Gly Ser Gly Ser Pro Leu Gly Leu Gly Thr Asp  
295 1 5 10 15  
297 (2) INFORMATION FOR SEQ ID NO: 8:  
299 (i) SEQUENCE CHARACTERISTICS:  
300 (A) LENGTH: 15 amino acids  
301 (B) TYPE: amino acid  
302 (D) TOPOLOGY: linear  
304 (ii) MOLECULE TYPE: peptide  
306 (v) FRAGMENT TYPE: internal  
310 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
312 Gly Leu Gly Thr Asp Ile Gly Gly Ser Ile Arg Phe Pro Ser Ala  
313 1 5 10 15  
315 (2) INFORMATION FOR SEQ ID NO: 9:  
317 (i) SEQUENCE CHARACTERISTICS:  
318 (A) LENGTH: 15 amino acids  
319 (B) TYPE: amino acid  
320 (D) TOPOLOGY: linear  
322 (ii) MOLECULE TYPE: peptide  
324 (v) FRAGMENT TYPE: internal  
328 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
330 Arg Phe Pro Ser Ala Phe Cys Gly Ile Cys Gly Leu Lys Pro Thr  
331 1 5 10 15  
333 (2) INFORMATION FOR SEQ ID NO: 10:  
335 (i) SEQUENCE CHARACTERISTICS:  
336 (A) LENGTH: 15 amino acids  
337 (B) TYPE: amino acid  
338 (D) TOPOLOGY: linear  
340 (ii) MOLECULE TYPE: peptide  
342 (v) FRAGMENT TYPE: internal  
346 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
348 Gly Leu Lys Pro Thr Gly Asn Arg Leu Ser Lys Ser Gly Leu Lys  
349 1 5 10 15  
351 (2) INFORMATION FOR SEQ ID NO: 11:  
353 (i) SEQUENCE CHARACTERISTICS:  
354 (A) LENGTH: 15 amino acids  
355 (B) TYPE: amino acid  
356 (D) TOPOLOGY: linear  
358 (ii) MOLECULE TYPE: peptide  
360 (v) FRAGMENT TYPE: internal  
364 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
366 Lys Ser Gly Leu Lys Gly Cys Val Tyr Gly Gln Thr Ala Val Gln  
367 1 5 10 15  
369 (2) INFORMATION FOR SEQ ID NO: 12:  
371 (i) SEQUENCE CHARACTERISTICS:  
372 (A) LENGTH: 15 amino acids  
373 (B) TYPE: amino acid  
374 (D) TOPOLOGY: linear  
376 (ii) MOLECULE TYPE: peptide

RAW SEQUENCE LISTING ERROR SUMMARY                    DATE: 09/17/2004  
PATENT APPLICATION: US/10/788,992                    TIME: 08:55:03

Input Set : N:\Crf3\RULE60\10788992.raw.txt  
Output Set: N:\CRF4\09172004\J788992.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 11,14,20  
Seq#:33; N Pos. 14  
Seq#:38; Xaa Pos.5  
Seq#:54; N Pos. 780,786,789,792,795,798,804,810,813,816,819

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/788,992

DATE: 09/17/2004

TIME: 08:55:03

Input Set : N:\Crf3\RULE60\10788992.raw.txt  
Output Set: N:\CRF4\09172004\J788992.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:35 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)  
L:957 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:35  
L:1222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:0